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1

SEQUENCE LISTING

#9

<110> Rastelli, Luca

Pennica, Diane

<120> NOVEL HUMAN STRA6-LIKE PROTEIN AND NUCLEIC ACIDS ENCODING THE SAME

<130> 10716/57

<140> 09/816,653

<141> 2001-03-23

<150> 60/191,532

<151> 2000-03-23

<160> 7

<170> PatentIn version 3.1

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<211> 598

<212> DNA

<213> Homo sapiens hSTRA6 nucleotide fragment, 5' region

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| agctggtaca | tcgatgagcc | ccaggggggg | gnngagctcc | agccagaggg | ggaagtgc | 120 |
| tcctgccaca | ccagcataacc | acccggcctg | taccacgcct | gcctggc | ctcgtcaatc | 180 |
| cttgtgtgc | tgctcctggc | catgctggtg | aggcgccg | agctctggcc | tgactgtgtg | 240 |
| cgtggcaggc | ccggcctg | cagccctgtg | gatttcttgg | ctggggacag | gccccgggca | 300 |
| gtgcctgctg | ctgtttcat | ggtcctcttg | agctccctgt | gtttgctg | ccccgacgag | 360 |
| gacgcattgc | cttcctgac | tctcg | gcacccagcc | aagatggaa | aactgaggct | 420 |
| ccaagagggg | cctggaagat | actgggactg | ttccattatg | ctgc | ctaccctctg | 480 |
| gctgcctgtg | ccacggctgg | ccacacagct | gcacac | tcggcagcac | gtgtcctgg | 540 |
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Gly Leu Tyr His Ala Cys Leu Ala Ser Leu Ser Ile Leu Val Leu Leu
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Leu Leu Ala Met Leu Val Arg Arg Arg Gln Leu Trp Pro Asp Cys Val
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Arg Gly Arg Pro Gly Leu Pro Ser Pro Val Asp Phe Leu Ala Gly Asp
85 90 95

Arg Pro Arg Ala Val Pro Ala Ala Val Phe Met Val Leu Leu Ser Ser
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Leu Cys Leu Leu Pro Asp Glu Asp Ala Leu Pro Phe Leu Thr Leu
115 120 125

Ala Ser Ala Pro Ser Gln Asp Gly Lys Thr Glu Ala Pro Arg Gly Ala
130 135 140

Trp Lys Ile Leu Gly Leu Phe His Tyr Ala Ala Leu Tyr Tyr Pro Leu
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Ala Ala Cys Ala Thr Ala Gly His Thr Ala Ala His Leu Leu Gly Ser
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Cys Pro Gln Val Pro Lys Ile
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| ccccaggaca gcctcagacc | agggggaggaa gacgaaggat gcagctgcta cagacaaagg | 660 |
| actccatggc caagggagct | aggccccgggg ccanccgcgg cagggctcgc tgggtctgg | 720 |
| cctacacgct gctgcacaac | ccaaccctgc aggtcttcg caagacggcc ctgttgggtg | 780 |
| ccaatggtgc ccagccctgc | tcctccctcc ccggctctcc tcccagcatac acaccagcca | 840 |
| tgcagccagc aggtcctccg | gatcacngtg gttnggtgga ggtctgtctg cactgggagc | 900 |
| ctcangangg ctctgctcca | cccacttggc tatgggagag ccagcaggggg ttctggagaa | 960 |
| aaaaactggt gggtagggc | cttggtccag gagccagttg agccagggca gccacatcca | 1020 |

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| Leu | Met | Arg | Ser | Leu | Val | Thr | His | Arg | Leu | Gly | Ser | Gly | Gly | Ser | Gly | |
| | | | | | | | | 20 | | 25 | | | | 30 | | |
| Asp | Gly | Gln | Phe | Ser | Trp | Asn | Leu | Phe | Ser | Val | Pro | Leu | Pro | Leu | Pro | |
| | | | | | | | | 35 | | 40 | | | | 45 | | |
| Pro | Leu | Ala | Gly | Leu | Leu | Val | Gln | Gln | Ile | Ile | Phe | Phe | Leu | Gly | Thr | |
| | | | | | | | | 50 | | 55 | | | | 60 | | |
| Thr | Ala | Leu | Ala | Phe | Leu | Val | Leu | Met | Pro | Val | Leu | His | Gly | Arg | Asn | |
| | | | | | | | | 65 | | 70 | | | | 75 | | 80 |
| Leu | Leu | Phe | Phe | Arg | Ser | Leu | Glu | Ser | Ser | Trp | Pro | Phe | Trp | Leu | Thr | |
| | | | | | | | | 85 | | 90 | | | | 95 | | |

Leu Ala Leu Ala Val Ile Leu Gln Asn Met Ala Ala His Trp Val Phe
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Leu Glu Thr His Asp Gly His Pro Gln Leu Thr Asn Arg Arg Val Leu
115 120 125

Tyr Ala Ala Thr Phe Leu Leu Phe Pro Leu Asn Val Leu Val Gly Ala
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Met Xaa Xaa Xaa Cys Ser Pro Ser Ile Ala Ile Arg His Pro Thr Pro
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Gly Tyr Tyr Thr Tyr Arg Asn Phe Leu Lys Ile Glu Val Ser Gln Ser
165 170 175

His Pro Ala Met Thr Ala Phe Cys Ser Leu Leu Leu Gln Ala Gln Ser
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Leu Leu Pro Arg Thr Met Ala Ala Pro Gln Asp Ser Leu Arg Pro Gly
195 200 205

Glu Glu Asp Glu Gly Met Gln Leu Leu Gln Thr Lys Asp Ser Met Ala
210 215 220

Lys Gly Ala Arg Pro Gly Ala Xaa Arg Gly Arg Ala Arg Trp Gly Leu
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Ala Tyr Thr Leu Leu His Asn Pro Thr Leu Gln Val Phe Arg Lys Thr
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Ala Leu Leu Gly Ala Asn Gly Ala Gln Pro Cys Ser Ser Leu Pro Gly
260 265 270

Ser Pro Pro Ser Ile Thr Pro Ala Met Gln Pro Ala Gly Pro Pro Asp
275 280 285

His Xaa Gly Xaa Val Glu Val Cys Leu His Trp Glu Pro Xaa Xaa Gly
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Lys Lys Leu Val Gly
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<212> DNA

<213> Homo sapiens clone RP11-60L3, Sequencing in Progress, 9 unordered pieces; GenBank AC023300, nts 150524 to 157487

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| gccagggagc agctcctggg caggggctgc taggtctggc tctgccactc atttgctgtg | 240 | |
| tgaccttggg caagtcacag cctctctggg gttcattcag tctctgcctc tgttacatga | 300 | |
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| gccccatagcc aggtatggaga agctgctgag agcagtttag gcaaggcagac ctcccttcaa | 480 | |
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Gln Ser His Pro Gly Val Ile Ala Phe Cys Ala Leu Leu Leu His Ala
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Pro Ser Pro Gln Pro Arg Pro Pro Leu Ala Pro Gln Asp Ser Leu Arg

595

600

605

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